

Access DB# 117502

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

\*\*\*\*\*

### STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>[Signature]</u>	NA Sequence (#) <input checked="" type="checkbox"/>	STN _____
Searcher Phone #: <u>122504</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>3/23</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>3/24</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>15</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>+15</u>	Other _____	Other (specify) _____



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 117502**

**TO: Phillip Gambel**  
**Location: 3e81 / 3c70**  
**Wednesday, March 24, 2004**  
**Art Unit: 1644**  
**Phone: 272-0844**  
**Serial Number: 09 / 955866**

**From: Jan Delaval**  
**Location: Biotech-Chem Library**  
**Rem 1A51**  
**Phone: 272-2504**  
**jan.delaval@uspto.gov**

### **Search Notes**

17502

**Delaval, Jan**

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**From:** Gambel, Phillip  
**Sent:** Tuesday, March 23, 2004 9:51 AM  
**To:** Delaval, Jan  
**Subject:** FW: roark amendment for new examiner 09/955,866

**Subject:** roark amendment for new examiner 09/955,866

Jan

Please perform a sequence and a sequence interference search for

USSN 09 / 955,866 (roark amendment for new examiner)

- 1) SEQ ID NO: 1
- 2) SEQ ID NO: 1 as an "oligo"
- 3) SEQ ID NO: 2
- 4) SEQ ID NO: 2 as an "oligo"

Thanx

Phillip Gambel  
Art Unit 1644  
272-0844

1644 mailbox 3c70

C 89	1.6	1200	9	US-09-887-576-694	Sequence 694, App	APPLICANT: Sullivan, John K.
C 90	1.6	1682	9	US-09-938-842A-4952	Sequence 4952, Ap	APPLICANT: Holst, Paige
C 91	1.6	1682	11	US-09-938-842A-4952	Sequence 4952, Ap	APPLICANT: Yoshinaga, Steven Kiyoshi
C 92	1.6	1711	12	US-10-112-944-144	Sequence 144, App	TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof
C 93	1.6	1725	9	US-09-818-143-19	Sequence 19, Appl	FILE REFERENCE: 00,759-A
C 94	1.6	1731	12	US-10-112-944-621	Sequence 621, App	CURRENT APPLICATION NUMBER: US/09/955,866
C 95	1.6	1990	14	US-10-198-846-9710	Sequence 9710, Ap	CURRENT FILING DATE: 2001-09-19
C 96	1.6	2013	13	US-09-920-300A-1665	Sequence 1665, Ap	PRIOR APPLICATION NUMBER: 60/233,867
C 97	1.6	2013	13	US-10-033-528-1665	Sequence 1665, Ap	PRIOR FILING DATE: 2000-09-20
C 98	1.6	2013	14	US-10-099-926-1665	Sequence 926, Ap	NUMBER OF SEQ ID NOS: 30
C 99	1.6	2041	15	US-10-108-260A-2338	Sequence 2338, Ap	SOFTWARE: PatentIn Ver. 2.0
C 100	1.6	75395	15	US-10-274-194-3	Sequence 3, Appl	SEQ ID NO 1
C 101	1.6	1691139	14	US-10-067-514-1	Sequence 1, Appl	LENGTH: 1209
C 102	1.6	1691139	15	US-10-419-723-1	Sequence 1, Appl	TYPE: DNA
C 103	1.5	18	9	US-09-875-338-67	Sequence 67, Appl	ORGANISM: Homo sapiens
C 104	1.5	18	9	US-09-875-338-68	Sequence 68, Appl	FEATURE:
C 105	1.5	18	9	US-09-875-338-72	Sequence 72, Appl	NAME/KEY: CDS
C 106	1.5	18	9	US-09-875-338-74	Sequence 74, Appl	LOCATION: (33)..(854)
C 107	1.5	18	9	US-09-875-338-77	Sequence 77, Appl	NAME/KEY: sig_peptide
C 108	1.5	18	9	US-09-875-338-79	Sequence 79, Appl	LOCATION: (33)..(89)
C 109	1.5	18	14	US-10-077-023-67	Sequence 67, Appl	NAME/KEY: misc feature
C 110	1.5	18	14	US-10-077-023-68	Sequence 68, Appl	LOCATION: (693)..(755)
C 111	1.5	18	14	US-10-077-023-72	Sequence 72, Appl	OTHER INFORMATION: predicted transmembrane domain
C 112	1.5	18	14	US-10-077-023-74	Sequence 74, Appl	US-09-955-866-1
C 113	1.5	18	14	US-10-077-023-77	Sequence 77, Appl	
C 114	1.5	18	14	US-10-077-023-79	Sequence 79, Appl	
C 115	1.5	26	9	US-09-875-338-90	Sequence 90, Appl	Query Match 100.0%; Score 1209; DB 9; Length 1209;
C 116	1.5	26	14	US-10-077-023-90	Sequence 90, Appl	Best Local Similarity 100.0%; Pred. No. 0;
C 117	1.5	101	15	US-10-260-937-42	Sequence 42, Appl	Matches 1209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C 118	1.5	220	12	US-10-425-114-3458	Sequence 3458, A	
C 119	1.5	332	10	US-09-918-998-6150	Sequence 6150, Ap	
C 120	1.5	481	12	US-10-424-599-31796	Sequence 31796, A	
C 121	1.5	481	15	US-10-027-632-182528	Sequence 182528, A	QY 1 CAGAAAGACCTATATGATCAAAATACAGAAATGATCTTCCTCTGCTAAATGTTGAGCC 60
C 122	1.5	481	15	US-10-027-632-182529	Sequence 182529, A	DB 1 CAGAAAGACCTATATGATCAAAATACAGAAATGATCTTCCTCTGCTAAATGTTGAGCC 60
C 123	1.5	481	15	US-10-027-632-182530	Sequence 182530, A	
C 124	1.5	499	12	US-10-085-783A-26103	Sequence 26103, A	QY 61 TGGAAITGACGCTTCCACAGATAGCAGCTTTATTCAGTGACAGCTCCCTAAGGAAGCTGT 120
C 125	1.5	499	15	US-10-242-538A-26103	Sequence 26103, A	DB 61 TGGAAITGACGCTTCCACAGATAGCAGCTTTATTCAGTGACAGCTCCCTAAGGAAGCTGT 120
C 126	1.5	537	15	US-10-191-803-860	Sequence 860, App	
C 127	1.5	568	12	US-10-424-599-121429	Sequence 121429, A	QY 121 ACNATATAGACATGCGACGATGTCACCTGGAAATGCAACTTTGACATCTGGAGGCTCATG 190
C 128	1.5	580	15	US-10-027-632-279438	Sequence 279438, A	DB 121 ACNATATAGACATGCGACGATGTCACCTGGAAATGCAACTTTGACATCTGGAGGCTCATG 190
C 129	1.5	585	15	US-10-027-632-194086	Sequence 194086, A	
C 130	1.5	585	15	US-10-027-632-219388	Sequence 219388, A	QY 181 TGAACCTTGGAGCAATAACAGCCAGCTTTGCAAAAGGTGGAATGATAATCATATCCCAACAC 240
C 131	1.5	637	15	US-10-027-632-227723	Sequence 227723, A	DB 181 TGAACCTTGGAGCAATAACAGCCAGCTTTGCAAAAGGTGGAATGATAATCATATCCCAACAC 240
C 132	1.5	637	15	US-10-027-632-227724	Sequence 227724, A	
C 133	1.5	657	15	US-10-027-632-240763	Sequence 240763, A	QY 241 GTCAAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCTTAGGAAAGGCTGTTCCACATAC 300
C 134	1.5	691	15	US-10-027-632-12094	Sequence 12094, A	DB 241 GTCAAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCTTAGGAAAGGCTGTTCCACATAC 300
C 135	1.5	728	9	US-09-910-943-738	Sequence 738, App	
C 136	1.5	734	15	US-10-027-632-150419	Sequence 150419, A	QY 301 CTCAGTCCCAAGTGGAGGAGGAGGACAGTACCAATGCATAATCATCTATGGGGTGGCCT 360
C 137	1.5	740	15	US-10-027-632-110077	Sequence 110077, A	DB 301 CTCAGTCCCAAGTGGAGGAGGAGGACAGTACCAATGCATAATCATCTATGGGGTGGCCT 360
C 138	1.5	785	12	US-10-425-114-5585	Sequence 5585, Ap	
C 139	1.5	868	14	US-10-195-730-83	Sequence 83, Appl	
C 140	1.5	1092	12	US-10-424-599-127452	Sequence 127452, A	QY 361 GGGACTACAGTACCTGACCTCTGAAAAGTCAAAAGCTTCCTACAGAAAATAAAACACTCACA 420
C 141	1.5	1169	14	US-10-198-846-10066	Sequence 10066, A	DB 361 GGGACTACAGTACCTGACCTCTGAAAAGTCAAAAGCTTCCTACAGAAAATAAAACACTCACA 420
C 142	1.5	1222	12	US-10-425-114-21572	Sequence 21572, A	
C 143	1.5	1338	12	US-10-282-122A-9428	Sequence 9428, Ap	QY 421 TCCTAAAGGTTCCAGAAAACAGATGAGGTAGAGTCACTACCTGCCAGGCTCAGGTTATCTTC 480
C 144	1.5	1392	12	US-10-425-114-5347	Sequence 5347, Ap	DB 421 TCCTAAAGGTTCCAGAAAACAGATGAGGTAGAGTCACTACCTGCCAGGCTCAGGTTATCTTC 480
C 145	1.5	1622	12	US-10-425-114-21515	Sequence 21515, A	
C 146	1.5	1626	9	US-09-764-877-2697	Sequence 2697, Ap	QY 481 TGGCAGAGTATCTCTGGCCAAACGTCAGGTTCTCTGCCAACACCCAGCCACTCCAGGACCC 540
C 147	1.5	1626	9	US-09-764-877-2699	Sequence 2699, Ap	DB 481 TGGCAGAGTATCTCTGGCCAAACGTCAGGTTCTCTGCCAACACCCAGCCACTCCAGGACCC 540
C 148	1.5	1626	15	US-10-264-049-95	Sequence 95, Appl	
C 149	1.5	1626	15	US-10-242-515-2687	Sequence 2687, Ap	QY 541 CTGAAGGCTCTACAGGTCACAGGTTCTGCGCTTAAGCCACCCCTGGGAGAACT 600
C 150	1.5	1626	15	US-10-242-515-2699	Sequence 2699, Ap	DB 541 CTGAAGGCTCTACAGGTCACAGGTTCTGCGCTTAAGCCACCCCTGGGAGAACT 600

## ALIGNMENTS

RESULT 1  
US-09-955-866-1  
; Sequence 1, Application US/09955966  
; Patent No. US20020107363A1  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Michael

Db 844 ACACAAACAAAGACCTGTACCAACAAAGAGGGAAGTGAACGTGATCTGAACCT 903  
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Db 1084 TTCACTGATCTGGACTCACCTCTGGAGCCTATGGCTTTAAGCAAGCACTACTGCACTTTA 1143  
QY 1099 CAGAATTACCCCACTGGATCCTGGACCCACAGAAATTCCTTCAGGATCCTTCTGGTGCCA 1158  
Db 1144 CAGAATTACCCCACTGGATCCTGGACCCACAGAAATTCCTTCAGGATCCTTCTGGTGCCA 1203  
QY 1159 GACTGAAAGCAAAAGGAATTAATTTCCCTCAAGTTTCTAAGTGATTTCCA 1209  
Db 1204 GACTGAAAGCAAAAGGAATTAATTTCCCTCAAGTTTCTAAGTGATTTCCA 1254

## RESULT 2

US-09-620-461-1  
; Sequence 1, Application US/09620461  
; Patent No. 6635750  
; GENERAL INFORMATION:  
; APPLICANT: Coyle, Anthony J.  
; APPLICANT: Fraser, Christopher C.  
; APPLICANT: Manning, Stephen  
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7  
; FILE OF INVENTION: Family and Uses Thereof  
; FILE REFERENCE: 5800-149  
; CURRENT APPLICATION NUMBER: US/09/620,461  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 2229  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(2229)  
; OTHER INFORMATION: n = A,T,C or G  
; NAME/KEY: CDS  
; LOCATION: (78)...(896)  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(2229)  
; OTHER INFORMATION: B7-2H Long  
US-09-620-461-1

Query Match 98.5%; Score 1191; DB 4; Length 2229;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 79 AGATAGCAGCTTTATTCACAGTGACAGTCCCTAAGCACTGTACATAATAGAGCATGGCA 138  
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QY 199 CAGCCAGTTTGCAAAAGCTGGAAATGATACATCCCAACACCGTGAAGAGCCACTTTGCG 258  
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Db 424 CTCTCAAACTCAAAAGCTTCTTACAGGAAATAAACAACACTCACATCTCTAAAGTTCAGAAA 483  
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## RESULT 3

US-09-910-174B-20

; Sequence 20, Application US/09910174B

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2004, 01:43:25 ; Search time 462 Seconds  
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9680.252 Million cell updates/sec

Title: US-09-955-866-1

Perfect score: 1209

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Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2438257 seqs, 1849576744 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database : Published Applications NA:\*

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18: /cgn2\_6/ptodata/2/pubna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1209	100.0	1209	US-09-955-866-1
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4	1191	98.5	2435	US-09-875-338-14
5	1191	98.5	2435	US-10-077-023-14
6	1155	95.5	2200	US-10-120-988-309
7	1140	94.3	2386	US-10-041-319-4
8	964	79.7	1223	US-09-895-837-1
9	964	79.7	1223	US-09-895-837-1
10	964	79.7	1223	US-10-034-650-41
11	891	73.7	2406	US-10-023-339-3
12	823	68.1	842	US-09-875-338-20
13	823	68.1	842	US-10-077-023-20
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15	822	68.0	822	US-10-034-650-42

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17	819	67.7	819	US-09-910-174A-20
18	819	67.7	819	US-09-895-837-3
19	819	67.7	819	US-09-896-913A-3
20	600	49.6	1356	US-09-875-338-16
21	600	49.6	1356	US-10-077-023-16
22	546	45.2	1975	US-09-910-174A-3
23	455	37.6	1675	US-10-023-339-10
24	361	29.9	549	US-09-910-174A-21
25	361	29.9	19217	US-09-955-866-18
26	361	29.9	79684	US-10-034-650-40
27	330	27.3	401	US-09-735-705-264
28	330	27.3	401	US-09-850-716A-264
29	330	27.3	401	US-09-897-778-264
30	330	27.3	401	US-10-117-982-264
31	330	27.3	401	US-10-313-986-264
32	324	26.8	660	US-10-029-020-31
33	309	25.6	9179	US-09-955-866-16
34	304	25.1	861	US-10-029-020-29
35	285	23.6	786	US-10-023-339-11
36	274	22.7	1814	US-09-955-866-17
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40	174	14.4	357	US-10-154-884B-3029
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74	21	1.7	5261	US-09-814-353-19577
75	20	1.7	20	US-09-875-338-85
76	20	1.7	20	US-09-875-338-86
77	20	1.7	20	US-10-029-020-170
78	20	1.7	20	US-10-077-023-85
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80	20	1.7	34	US-09-910-174A-26
81	20	1.7	194	US-10-085-783A-4002
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83	19	1.6	484	US-09-815-343-1319
84	19	1.6	484	US-10-097-105-1319
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86	19	1.6	650	US-10-027-632-193797
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XX	Abd59547	Connectiv	Abd59547	Connectiv	Abd59547	Connectiv	Abd59547							
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FT	Aas83126	DNA enco	Aas83126	DNA enco	Aas83126	DNA enco	Aas83126							
FT	Aax30464	H. pylori	Aax30464	H. pylori	Aax30464	H. pylori	Aax30464							
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XX	Aal42463	Human mat	Aal42463	Human mat	Aal42463	Human mat	Aal42463							
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XX	Adc20642	Human sec	Adc20642	Human sec	Adc20642	Human sec	Adc20642							
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XX	Aal26460	Human bre	Aal26460	Human bre	Aal26460	Human bre	Aal26460							
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XX	Abx93648	Human gen	Abx93648	Human gen	Abx93648	Human gen	Abx93648							
DR	Abq88101	Human ost	Abq88101	Human ost	Abq88101	Human ost	Abq88101							
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XX	Abk24091	B7-relate	Abk24091	B7-relate	Abk24091	B7-relate	Abk24091							
XX	Abd27953	Canine CO	Abd27953	Canine CO	Abd27953	Canine CO	Abd27953							
CC	Aai83753	Human pol	Aai83753	Human pol	Aai83753	Human pol	Aai83753							
CC	Ach18938	Human adu	Ach18938	Human adu	Ach18938	Human adu	Ach18938							
CC	Abn73636	Bovine em	Abn73636	Bovine em	Abn73636	Bovine em	Abn73636							
CC	Aad41728	Murine ri	Aad41728	Murine ri	Aad41728	Murine ri	Aad41728							
CC	Aai80602	Human pol	Aai80602	Human pol	Aai80602	Human pol	Aai80602							
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CC	Aai95488	Human neu	Aai95488	Human neu	Aai95488	Human neu	Aai95488							
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CC	Aah48396	Fumarase	Aah48396	Fumarase	Aah48396	Fumarase	Aah48396							
CC	Abx90530	Human CDN	Abx90530	Human CDN	Abx90530	Human CDN	Abx90530							
CC	Aad54709	Mouse SCR	Aad54709	Mouse SCR	Aad54709	Mouse SCR	Aad54709							
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19-SEP-2001; 2001WO-US029183.														
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20-SEP-2000; 2000US-0233867P.														
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(AMGE-) AMGEN INC.														
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Fox M, Sullivan JK, Holst P, Yoshinaga SK;														
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WPI; 2002-416284/44.														
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2004, 22:59:39 ; Search time 516 Seconds

(without alignment)  
9953.627 Million cell updates/sec

Title: US-09-955-866-1

Perfect score: 1209

Sequence: 1 cagaagagacattatgat.....agtttttaagtgatttoca 1209

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

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- 2: geneseqn1990s.\*
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- 6: geneseqn2002s.\*
- 7: geneseqn2003bs.\*
- 8: geneseqn2003cs.\*
- 9: geneseqn2003cs.\*
- 10: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1191	98.5	2229	6	AAD30541 Human B7-
3	1191	98.5	2229	6	AAL50534 Human B7-
4	1191	98.5	2386	7	AAD48356 Human B7-
5	1191	98.5	2435	6	ABK24017 DNA encod
6	1155	95.5	2200	7	ABX71082 Novel hum
7	1140	94.3	2386	7	AAD48333 Human B7-
8	1089	90.1	2386	7	AAD48354 Human B7-
9	964	79.7	1223	6	AAD27371 Human PD-
10	964	79.7	1223	6	AAL41871 Human PD-
11	964	79.7	1223	7	ABT14005 Human PD-
12	964	79.7	1223	7	ABX13050 Human PD-
13	964	79.7	1223	8	ADA03075 Human hCG
14	964	79.7	1223	8	ADA66359 Human hCG
15	964	79.7	1223	9	ADB72813 Human hCG
16	891	73.7	2406	4	AAD05220 Human sec
17	891	73.7	2406	6	AAD32520 Human B7-
18	891	73.7	2406	7	ADA55940 Gene enco
19	823	68.1	842	6	ABK24021 B7-relate
20	822	68.0	822	7	AAD48353 Human B7-
21	822	68.0	822	8	ADA03076 Human hCG
22	822	68.0	822	8	ADA66360 Human hCG
23	822	68.0	822	9	ADB72814 Human hCG

24	819	67.7	819	6	AAL50536	AAL50536 Human B7-
25	819	67.7	819	6	ABK88228	DNA encod
26	819	67.7	819	6	AAI70887	Human co-
27	785	64.9	1285	3	AAC59828	Human sec
28	779	64.4	1819	4	AAH14818	Human CDN
29	771	63.8	822	7	AAD48355	Human B7-
30	600	49.6	1356	6	ABK24018	DNA encod
31	558	46.2	793	4	AAH07485	Human CDN
32	546	45.2	1975	6	AAD30542	Human B7-
33	546	45.2	1975	6	AAL50535	Human B7-
34	455	37.6	1675	4	AAD05241	Human sec
35	455	37.6	1675	6	AAD32527	Human B7-
36	455	37.6	1675	7	ADA56467	Gene enco
37	361	29.9	549	6	AAL50537	Human B7-
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39	361	29.9	79684	8	ADA03074	Human hCG
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41	361	29.9	79684	9	ADB72812	Human hCG
42	330	27.3	401	3	AAC65960	Human lun
43	330	27.3	401	6	ABL49179	Human lun
44	330	27.3	401	6	ABQ92365	Human lun
45	330	27.3	401	8	ADA28354	Human lun
46	324	26.8	660	6	ABS52109	Human but
47	309	25.6	9179	6	AAD36971	Human B7-
48	304	25.1	861	6	ABS52108	Human but
49	285	23.6	786	4	AAD05242	Human sec
50	285	23.6	786	6	AAD32528	Human B7-
51	285	23.6	786	7	ADA56468	Gene enco
52	274	22.7	1814	6	AAD36972	Human B7-
53	70	5.8	7819	6	AAD36969	Human B7-
54	35	2.9	744	6	AAD30547	Murine or
55	35	2.9	744	8	AAL50543	Murine B7
56	35	2.9	744	8	ADA03073	Mouse mCG
57	35	2.9	744	8	ADA03072	Mouse mCG
58	35	2.9	744	8	ADA66357	Mouse mCG
59	35	2.9	744	8	ADA66356	Mouse mCG
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61	35	2.9	744	9	ADB72811	Mouse mCG
62	35	2.9	1655	6	AAD27372	Mouse PD-
63	35	2.9	1655	6	AAL41872	Mouse PD-
64	35	2.9	1655	6	AAI70888	Mouse co-
65	35	2.9	1655	7	ABX13051	Murine PD
66	35	2.9	78028	8	ADA03071	Mouse mCG
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69	27	2.2	27	6	AAD36974	Human B7-
70	26	2.2	26	6	AAD36977	Human B7-
71	25	2.1	25	6	AAD36976	Human B7-
72	25	2.1	34	6	ABK24082	B7-relate
73	25	2.1	34	6	ABK24090	B7-relate
74	24	2.0	31	6	ABK24092	B7-relate
75	23	1.9	23	6	ABS52198	Human pro
76	23	1.9	23	6	AAD27375	Human exp
77	23	1.9	23	6	AAD36975	Human B7-
78	23	1.9	23	6	AAL41881	Human PD-
79	23	1.9	23	7	ABX13054	Human PD-
80	23	1.9	33	6	ABK24083	B7-relate
81	22	1.8	22	6	ABK24081	B7-relate
82	22	1.8	22	6	AAD27376	Human exp
83	22	1.8	22	6	AAL41882	Human PD-
84	22	1.8	22	6	ABK88229	Human den
85	22	1.8	22	7	ABX13055	Human PD-
86	21	1.7	21	3	AAC59887	Oligonuc1
87	21	1.7	21	6	ABS52199	Human rev
88	21	1.7	21	6	ABK88230	Human den
89	21	1.7	38	6	AAD30544	Human B7-
90	21	1.7	38	6	AAL50540	Human B7-
91	21	1.7	482	8	ACH28752	Human adu
92	20	1.7	20	6	ABS52197	Human for
93	20	1.7	20	6	ABK24086	B7-relate
94	20	1.7	20	6	ABK24087	B7-relate
95	20	1.7	34	6	AAD30545	Human B7-
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2004, 00:06:30 ; Search time 2997 Seconds

(without alignments)  
12046.505 Million cell updates/sec

Title: US-09-955-866-1

Perfect score: 1209

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Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

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16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

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23: em\_gss\_nus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

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28: gb\_gsl:\*

29: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	232	19.2	940	13	BQ880729
6	228	18.9	502	13	EX280151
7	199	16.5	279	9	AA303575
c 8	184	15.2	638	29	AG087778
c 9	170	14.1	356	10	AW889458
c 10	148	12.2	526	28	AO691335
c 11	123	10.2	775	14	CB312518
c 12	105	8.7	240	9	AA247128
c 13	105	8.7	404	9	AA247117
c 14	99	8.2	573	9	AI762460
c 15	91	7.5	390	9	AA036918
c 16	35	2.9	1533	11	AK089369
c 17	24	2.0	661	13	BY749628
c 18	22	1.8	633	29	CE441123
c 19	22	1.8	650	28	BZ836208
c 20	22	1.8	791	29	CC921818
c 21	22	1.8	824	13	BU748640
c 22	22	1.8	1029	13	BU746079
c 23	21	1.7	93	28	AZ812514
c 24	21	1.7	314	14	T05423
c 25	21	1.7	332	10	BE111013
c 26	21	1.7	439	14	CF137914
c 27	21	1.7	456	14	CB545564
c 28	21	1.7	750	14	CF744925
c 29	21	1.7	771	10	BE883693
c 30	21	1.7	799	14	W28577
c 31	21	1.7	849	13	BQ231790
c 32	21	1.7	858	12	BG291661
c 33	21	1.7	868	12	BG282544
c 34	21	1.7	917	9	AL556281
c 35	21	1.7	1018	10	BE962915
c 36	21	1.7	1059	12	BM464169
c 37	21	1.7	1134	12	BM461393
c 38	20	1.7	250	9	AI758557
c 39	20	1.7	286	9	AI272169
c 40	20	1.7	385	29	CE357725
c 41	20	1.7	404	9	AA037029
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c 43	20	1.7	416	28	AQ806377
c 44	20	1.7	443	14	CB789448
c 45	20	1.7	493	9	AA442937
c 46	20	1.7	517	28	AQ315307
c 47	20	1.7	545	10	BG009657
c 48	20	1.7	553	9	AUI69804
c 49	20	1.7	560	12	BG989592
c 50	20	1.7	564	28	CE409086
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c 52	20	1.7	615	12	BG525719
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ALIGNMENTS

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; Patent No. 6630575  
; GENERAL INFORMATION:  
; APPLICANT: Coyle, Anthony J.  
; APPLICANT: Fraser, Christopher C.  
; APPLICANT: Manning, Stephen  
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7  
; FILE REFERENCE: 35800/236924  
; CURRENT APPLICATION NUMBER: US/09/910,174B  
; CURRENT FILING DATE: 2003-07-20  
; PRIOR APPLICATION NUMBER: US 09/620,461  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1

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OM nucleic - nucleic search, using sw model

Run on: March 24, 2004, 00:04:09 ; Search time 117 Seconds  
(without alignments)

5734.493 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	546	45.2	1975	4	US-09-910-174B-3
7	361	29.9	549	4	US-09-910-174B-21
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26	17	1.4	591	2	US-08-704-473-1
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96	16	1.3	1001	4	US-09-533-029-45
97	16	1.3	1006	4	US-08-956-171E-386
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99	16	1.3	1152	3	US-09-188-930-42
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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11182.614 Million cell updates/sec

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Word size: 0

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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6	1191	98.5	2229	6	AX357968 Sequence
7	1140	94.3	2386	6	AX698931 Sequence
8	964	79.7	1223	6	AX420002 Sequence
9	964	79.7	1223	6	AX460797 Sequence
10	964	79.7	1223	6	AX695966 Sequence
11	964	79.7	1223	9	AF344424 Homo sapi
12	823	68.1	842	6	AX357974 Sequence
13	822	68.0	822	6	AX695967 Sequence
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15	822	68.0	822	9	AY254343 Sequence
16	819	67.7	819	6	AR407783 Sequence
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25	779	64.4	1819	9	AK001872 Homo sapi
26	600	49.6	1356	6	AX357970 Sequence
27	558	46.2	793	6	AX869415 Sequence
28	558	46.2	793	6	BD149477 Primer fo
29	546	45.2	1975	6	AR407782 Sequence
30	546	45.2	1975	6	AR411238 Sequence
31	546	45.2	1975	6	AX370288 Sequence
32	361	29.9	549	6	AR407784 Sequence
33	361	29.9	549	6	AR411240 Sequence
34	361	29.9	549	6	AX370306 Sequence
35	361	29.9	19217	6	AX411791 Sequence
36	361	29.9	79684	6	AX695965 Sequence
37	361	29.9	146327	9	AL162253 Human DNA
38	330	27.3	401	6	BD275827 COMPOUNDS
39	330	27.3	401	6	AR220612 Sequence
40	330	27.3	401	6	AR255606 Sequence
41	330	27.3	401	6	AR281176 Sequence
42	330	27.3	401	6	AX365871 Sequence
43	324	26.8	660	6	AX556518 Sequence
44	309	25.6	9179	6	AX411789 Sequence
45	304	25.1	861	6	AX556516 Sequence
46	274	22.7	1814	6	AX411790 Sequence
47	70	5.8	1799	9	AK093681 Homo sapi
48	70	5.8	7819	6	AX411787 Sequence
49	45	3.7	245032	2	AC096309 Rattus no
50	45	3.7	261001	2	AC096324 Rattus no
51	35	2.9	741	6	AX420007 Sequence
52	35	2.9	741	6	AX460802 Sequence
53	35	2.9	744	6	AR407790 Sequence
54	35	2.9	744	6	AX354741 Sequence
55	35	2.9	744	6	AX370315 Sequence
56	35	2.9	744	6	AX695963 Sequence
57	35	2.9	744	6	AX695964 Sequence
58	35	2.9	1655	6	AX354739 Sequence
59	35	2.9	1655	6	AX420005 Sequence
60	35	2.9	1655	6	AX460800 Sequence
61	35	2.9	1655	10	AF142780 Mus muscu
62	35	2.9	78028	6	AX695962 Sequence
63	35	2.9	308353	2	AC093339 Mus muscu
64	27	2.2	27	6	AX411799 Sequence
65	26	2.2	26	6	AX411803 Sequence

Pred. No. is the number of results predicted by chance to have a